We claim:

1. A method, comprising:

(a) incubating a reaction mixture comprising:

(i) a sample nucleic acid obtained from a biological sample suspected of containing a TIGR nucleic acid sequence,

(ii) a nucleic acid polymerase,

(iii) one or more extension primers that specifically bind to said TIGR nucleic acid sequence if present, and that, when extended by one nucleotide at the 3' end, comprise a nucleotide indicative of one or more preselected polymorphisms in said TIGR nucleic acid sequence, and

(iv) one or more labeled ddNTPs,

under conditions such that, in the presence of said TIGR nucleic acid sequence, said extension primer(s) are distinctively labeled by addition of one of said labeled ddNTP(s) to the 3'-end of said detection primer, to generate a labeled nucleic acid corresponding to one of said preselected polymorphism(s); and

(b) detecting a signal from said labeled nucleic acid, wherein said signal is related to a TIGR genotype present in said sample.

2. The method of claim 1, wherein said sample nucleic acid is obtained by amplification of nucleic acid in said biological sample.

3. The method of claim 2, wherein nucleic acid in said biological sample is amplified by a polymerase chain reaction.

4. The method of claim 3, wherein nucleic acid in said sample is amplified using one or more amplification primer sequences selected from the group consisting of SEQ ID NOS:5-8

5. The method of claim 1, wherein step (b) comprises separating said labeled nucleic acid(s) by electrophoresis.

6. The method of claim 5, wherein said electrophoresis is capillary electrophoresis.

7. The method claim 1, wherein steps (a) and (b) are performed by automated means.

8. The method of claim 1, wherein said labeled ddNTPs are fluorescently labeled.

9. The method of claim 1, wherein said labeled ddNTPs comprise ddCTP, ddGTP, ddATP and ddTTP, each of which are physically distinguishable from one another.

10. The method of claim 9, wherein comprise ddCTP, ddGTP, ddATP and ddTTP, each comprise a different fluorescent label.

11. The method of claim 1, wherein said preselected polymorphisms in said TIGR gene sequence are selected from the group consisting of MT-1, T377M, E423K, and N480K.

12. The method of claim 1, wherein said extension primers consist of an oligonucleotide 17-50 bases in length, comprising at the 3' end a sequence selected from the group consisting of SEQ ID NOS: 1-4.

13. The method of claim 1, wherein said biological sample is a human sample.

14. The method of claim 13, wherein said human sample is obtained by scraping within the buccal cavity.

15. A method of identifying a subject at increased risk for developing primary open angle glaucoma, comprising:

correlating a TIGR genotype of said subject identified by the method of claim 1 to a relative risk of developing primary open angle glaucoma associated with said TIGR genotype.

16. A method of selecting a treatment regimen for a subject, said method comprising:

selecting said treatment regimen to be compatible with a TIGR genotype of said subject identified by the method of claim 1.

17. An oligonucleotide consisting essentially of a sequence selected from the group consisting of SEQ ID NOS: 1-8.

18. The oligonucleotide of claim 15, wherein said oligonucleotide is substantially pure.

19. A kit, comprising:

one or more extension primers consisting of an oligonucleotide 17-50 bases in length, comprising at the 3' end a sequence selected from the group consisting of SEQ ID NOS: 1-4; and

instructions for performing a method using said one or more extension primers to perform said assay.

20. The kit of claim 19, wherein said extension primer(s) are selected from the group consisting of SEQ ID NOS: 1-4.

21. The kit of claim 17, further comprising one or more amplification primers having sequences selected from the group consisting of SEQ ID NOS: 5-8.